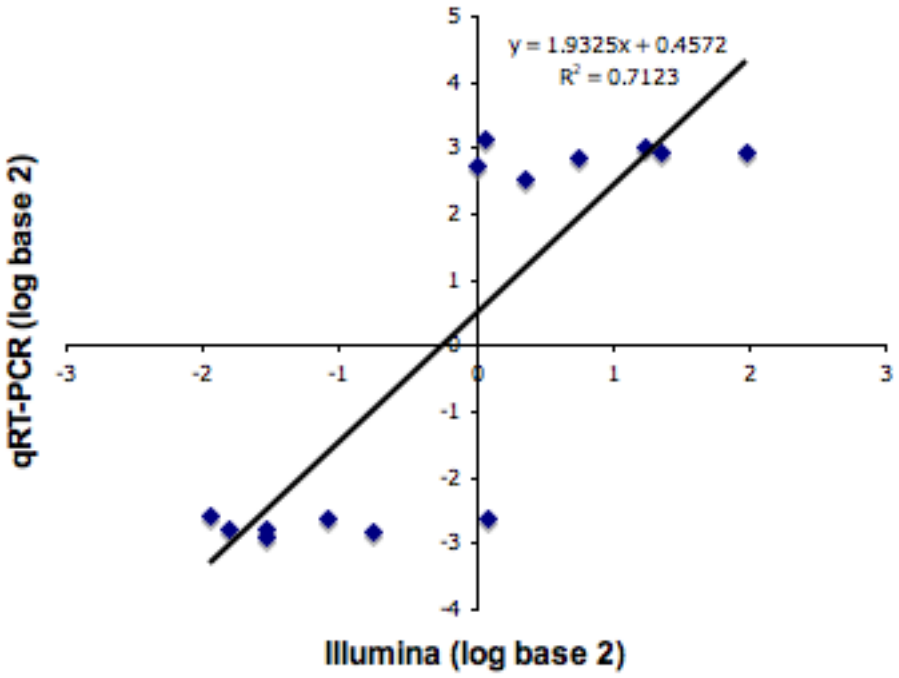
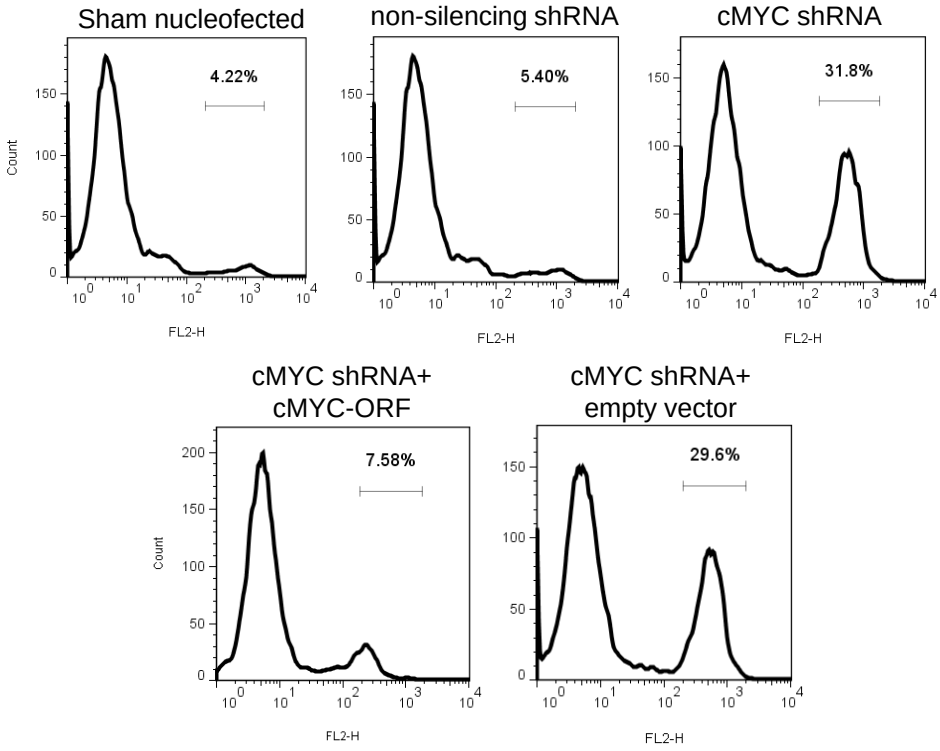
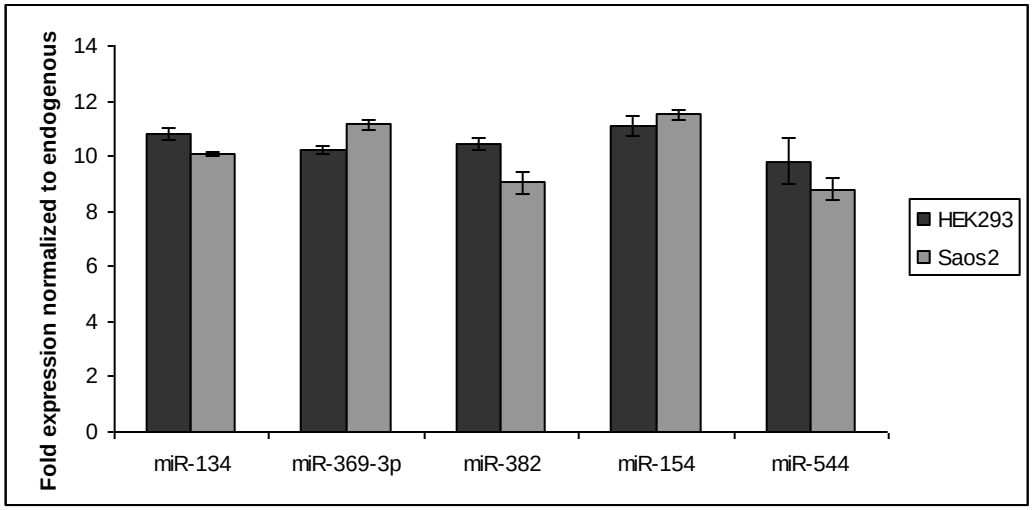
Supplemental Figures



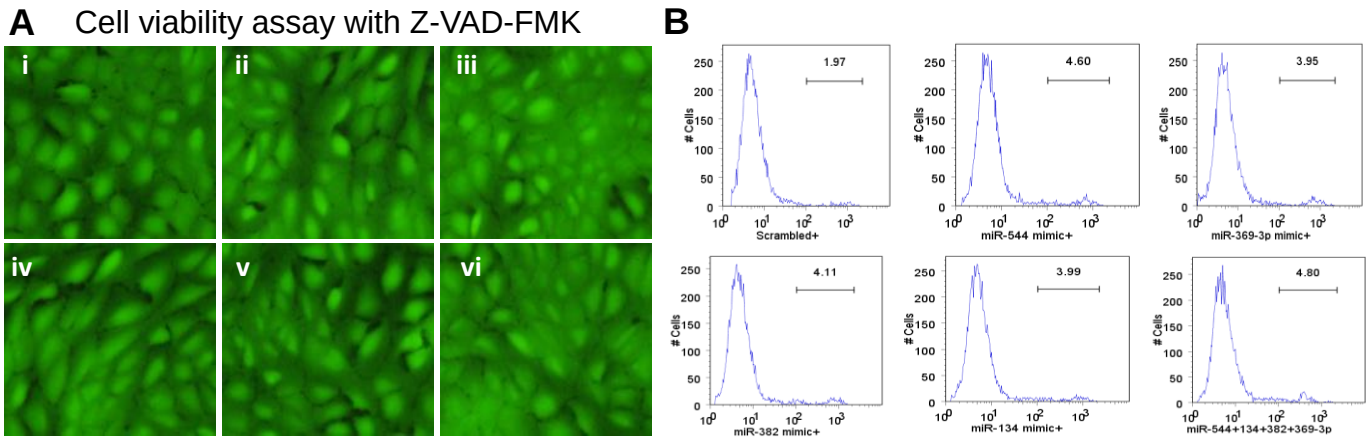
Supplementary Figure 1. Correlation between gene expression detected by illumina microRNA array and qRT-PCR for 14q32 miRNAs and miR-17-92.



Supplementary Figure 2: Depletion of endogenous *cMYC* through RNAi induce apoptosis in U2os cells



Supplementary Figure 3. Expression levels of 14q32 miRs in HEK293 and Saos2 cells 48 hrs after delivery of microRNA mimics. Levels were quantified by qRT-PCR and shown relative to endogenous expression.



Supplementary Figure 4. Cell viability assay (A) and FACS analysis (B) of nucleofected Saos2 cells. 14q32 miRNAs promote apoptotic cell death. Cells were treated as in panel A, except that they were cultured in medium containing the caspase inhibitor Z-VAD-fmk. (B).

Supplementary Figure 5.

Differential expression of genes in OS patients and OS cell lines, relative to normal bone (FT-406 and 407).

MEG3 (located on 14q32) and NOTCH genes are down regulated in OS patients and OS cell lines compared to normal bone. On the contrary, cell cycle related genes such as CCNA2, AURKA and AURKB are upregulated in OS relative to normal bone. TWIST1, Runx2, CDC5L and CCNA2 are induced in the metastatic OS cell lines LM2 and LM7, relative to Saos2.